*Poster*

# Study of phytopathogenesis regulation through chromatine modification


Fernández Portillo, Ismael and Ramos Barrales, Ramón (1)

1. Área de Genética, Centro Andaluz de Biología del Desarrollo, Ctra. de Utrera, km. 1, 41013, Sevilla.

Tutor académico: Ramón Ramos Barrales (1)

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## ABSTRACT

Chromatin is a structure formed by DNA and protein found in eukaryotic cells. This structure serves to package and condense the DNA. Histones are the main proteins forming part of this structure. The histones have aminoacidic tails which modifications are highly involved in transcriptional control of genetic programs that lead essentials processes like mitosis or more complex processes as can be cell differentiation. We have done a phylogenetic study and have found 3 genes which can encode the enzymes in charge of histone H3 methylation at its lysine resides 9 (KMT1) and 36 (KMT3 and KMT2H). The lysine 9 methylation in H3 is the main hallmark of constitutive heterochromatin (1,2) and the H3 lysine 36 methylation is generally associated with active transcription (3). We have deleted these putative methyltransferases in Ustilago maydis. While KMT1 deletion has not showed a significant virulence phenotype, both H3K36 methyltransferases mutants present infection defects. Interestingly, meanwhile KMT3 deletion shows a reduction in virulence, KMT2H deletion improve pathogenesis. In addition, by western blot analysis we have observed a reduction of H3K36 trimethylation in both mutants respect the wild type strain, indicating there are two H3K36 methyltransferases with opposite roles in infection. These observations are in agreement with a recent publication where the fungus Fusarium fujikuroi is methylating H3K36 in heterochromatin and euchromatin area through two different methyltransferases (4). We are currently studying the differences between these methyltrasnferases at the molecular and cellular level during the pathogenesis process.

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